

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/568,332  
Source: IFWP  
Date Processed by STIC: 2/27/06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 02/27/2006

PATENT APPLICATION: US/10/568,332

TIME: 14:53:36

Input Set : F:\61310.us.sequences.ST25.txt

Output Set: N:\CRF4\02272006\J568332.raw

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3 <110> APPLICANT: Stempfer, Gunter
4     Alliger, Peter
5     Palma, Norbert
7 <120> TITLE OF INVENTION: Process for the purification of recombinant
polypeptides
9 <130> FILE REFERENCE: BP/G-33315A LNG 61310.US
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/568,332
C--> 11 <141> CURRENT FILING DATE: 2006-02-13
11 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/009055
12 <151> PRIOR FILING DATE: 2004-08-12
14 <150> PRIOR APPLICATION NUMBER: US 60/494,915
15 <151> PRIOR FILING DATE: 2003-08-13
17 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 23
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Primer
29 <400> SEQUENCE: 1
30 taactgtcag accaagttta ctc                                     23
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34 <211> LENGTH: 20
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Primer
41 <400> SEQUENCE: 2
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45 <210> SEQ ID NO: 3
46 <211> LENGTH: 23
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial
50 <220> FEATURE:
51 <223> OTHER INFORMATION: Primer
53 <400> SEQUENCE: 3
54 tcatgtttga cagcttatca tcg                                     23
57 <210> SEQ ID NO: 4
58 <211> LENGTH: 19
59 <212> TYPE: DNA
60 <213> ORGANISM: Artificial
62 <220> FEATURE:
63 <223> OTHER INFORMATION: Primer

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65 <400> SEQUENCE: 4
66 ggtcgaggtg gcccggtc 19
69 <210> SEQ ID NO: 5
70 <211> LENGTH: 27
71 <212> TYPE: PRT
72 <213> ORGANISM: Pseudomonas diminuta
74 <400> SEQUENCE: 5
76 Met Leu Arg Val Leu His Arg Ala Ala Ser Ala Leu Val Met Ala Thr
77 1 5 10 15
80 Val Ile Gly Leu Ala Pro Ala Val Ala Phe Ala
81 20 25
84 <210> SEQ ID NO: 6
85 <211> LENGTH: 36
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Primer
92 <400> SEQUENCE: 6
93 ggggggtcta gaccaacaac atcttcaacg tctacc 36
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 32
98 <212> TYPE: DNA
99 <213> ORGANISM: Artificial
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Primer
104 <400> SEQUENCE: 7
105 cccccgaat tcaactagtagt gcgtctctct cc 32
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 315
110 <212> TYPE: DNA
111 <213> ORGANISM: Artificial
113 <220> FEATURE:
114 <223> OTHER INFORMATION: gac fragment
116 <400> SEQUENCE: 8
117 ggggggtcta gaccaacaac atcttcaacg tctaccgac caagattcag gagccgtcgg 60
119 ccgacctggg caatgggatg tacagcgggc ttgcgccgtt cggcttcacc ggcggatcct 120
121 gggttcgtacg cgccgctac aagtggatg ctagggggaac gttccggggg cgtcgtgca 180
123 acggcgtctc cggatctggg tgagagggga aatccatgct gagagtctg caccgggcgg 240
125 cgtccgcctt gggtatggcg actgtgatcg gccttgccgc ccgaggagaga gacgcgtact 300
127 agtgaattcg ggggg 315
130 <210> SEQ ID NO: 9
131 <211> LENGTH: 11
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Sac II site
138 <400> SEQUENCE: 9
139 tcgcctttgc g 11
142 <210> SEQ ID NO: 10

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143 <211> LENGTH: 23
144 <212> TYPE: DNA
145 <213> ORGANISM: Artificial
147 <220> FEATURE:
148 <223> OTHER INFORMATION: Primer
150 <400> SEQUENCE: 10
151 ttgcgcccgc ggtcgcttt gcg                                     23
154 <210> SEQ ID NO: 11
155 <211> LENGTH: 4
156 <212> TYPE: PRT
157 <213> ORGANISM: Artificial
159 <220> FEATURE:
160 <223> OTHER INFORMATION: gac signal sequence
162 <400> SEQUENCE: 11
164 Val Ala Phe Ala
165 1
168 <210> SEQ ID NO: 12
169 <211> LENGTH: 540
170 <212> TYPE: DNA
171 <213> ORGANISM: Artificial
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Interferon alpha structural gene fragment
176 <400> SEQUENCE: 12
177 ggggggcccgc ggtcgcttt gcgtgcgac tgccgcaaac ccacagcctg ggtagccggc      60
179 gaaccttgat gcttctggca cagatgcggc gaatctctct tttctcttgc ttaaaggatc    120
181 gacatgactt cggtttcccg caggaggagt tcggtaacca gttccaaaag gctgaaacca    180
183 tcccggtatt gcatgagatg atccagcaga tcttcaacct gttcagcact aaggactctt    240
185 ctgctgcttg ggatgagacc ctgcttgaca aattctacac tgaactgtac cagcagctga    300
187 acgacctgga agcctgcgtg atccaggggtg tgggtgtgac tgagactccg ctgatgaagg    360
189 aggactctat tctggctgtg cgaaaatact tccaacggat cactctgtat ctgaaagaga    420
191 agaaatacag cccgtgcgcc tgggagggtt tccgagcaga aatcatgcgg tctttctctt    480
193 tgtctaccaa cttgcaagaa tctttacgaa gcaaggaata atacgcgtga attcgggggg    540
196 <210> SEQ ID NO: 13
197 <211> LENGTH: 807
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial
201 <220> FEATURE:
202 <223> OTHER INFORMATION: gene encoding a gac1ss-rhIFNa2b fusion protein
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (210)..(788)
209 <400> SEQUENCE: 13
210 tctagaccaa caacatcttc aacgtctacc cgaccaagat tcaggagccg tcggccgacc      60
212 tgggcaatgg gatgtacagc gggcttgcgc cgttcggctt caccggcgga tcctgggtcg    120
214 tacgcgccgc ctacaagtgg tgatctaggg gaacgttccg ggggcgtcgc tgcaacggcg    180
216 tctccggatc tgggtgagag gggaaatcc atg ctg aga gtt ctg cac cgg gcg      233
217                                     Met Leu Arg Val Leu His Arg Ala
218                                     1                               5
220 gcg tcc gcc ttg gtt atg gcg act gtg atc ggc ctt gcg ccc gcg gtc      281

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221 Ala Ser Ala Leu Val Met Ala Thr Val Ile Gly Leu Ala Pro Ala Val
222      10      15      20
224 gcc ttt gcg tgc gat ctg ccg caa acc cac agc ctg ggt agc cgg cga      329
225 Ala Phe Ala Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg
226 25      30      35      40
228 acc ttg atg ctt ctg gca cag atg cgg cga atc tct ctt ttc tct tgc      377
229 Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys
230      45      50      55
232 tta aag gat cga cat gac ttc ggt ttc ccg cag gag gag ttc ggt aac      425
233 Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn
234      60      65      70
236 cag ttc caa aag gct gaa acc atc ccg gta ttg cat gag atg atc cag      473
237 Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln
238      75      80      85
240 cag atc ttc aac ctg ttc agc act aag gac tct tct gct gct tgg gat      521
241 Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp
242      90      95      100
244 gag acc ctg ctt gac aaa ttc tac act gaa ctg tac cag cag ctg aac      569
245 Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn
246 105      110      115      120
248 gac ctg gaa gcc tgc gtg atc cag ggt gtg ggt gtg act gag act ccg      617
249 Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro
250      125      130      135
252 ctg atg aag gag gac tct att ctg gct gtg cga aaa tac ttc caa cgg      665
253 Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg
254      140      145      150
256 atc act ctg tat ctg aaa gag aag aaa tac agc ccg tgc gcc tgg gag      713
257 Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu
258      155      160      165
260 gtt gtc cga gca gaa atc atg cgg tct ttc tct ttg tct acc aac ttg      761
261 Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu
262      170      175      180
264 caa gaa tct tta cga agc aag gaa taa tacgcgtact agtgaattc      807
265 Gln Glu Ser Leu Arg Ser Lys Glu
266 185      190
269 <210> SEQ ID NO: 14
270 <211> LENGTH: 192
271 <212> TYPE: PRT
272 <213> ORGANISM: Artificial
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Synthetic Construct
277 <400> SEQUENCE: 14
279 Met Leu Arg Val Leu His Arg Ala Ala Ser Ala Leu Val Met Ala Thr
280 1      5      10      15
283 Val Ile Gly Leu Ala Pro Ala Val Ala Phe Ala Cys Asp Leu Pro Gln
284      20      25      30
287 Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met
288      35      40      45
291 Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly

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292	50		55		60											
295	Phe	Pro	Gln	Glu	Glu	Phe	Gly	Asn	Gln	Phe	Gln	Lys	Ala	Glu	Thr	Ile
296	65					70					75				80	
299	Pro	Val	Leu	His	Glu	Met	Ile	Gln	Gln	Ile	Phe	Asn	Leu	Phe	Ser	Thr
300					85					90					95	
303	Lys	Asp	Ser	Ser	Ala	Ala	Trp	Asp	Glu	Thr	Leu	Leu	Asp	Lys	Phe	Tyr
304				100					105					110		
307	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	Asp	Leu	Glu	Ala	Cys	Val	Ile	Gln
308			115					120					125			
311	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	Leu	Met	Lys	Glu	Asp	Ser	Ile	Leu
312		130					135				140					
315	Ala	Val	Arg	Lys	Tyr	Phe	Gln	Arg	Ile	Thr	Leu	Tyr	Leu	Lys	Glu	Lys
316	145					150					155				160	
319	Lys	Tyr	Ser	Pro	Cys	Ala	Trp	Glu	Val	Val	Arg	Ala	Glu	Ile	Met	Arg
320					165					170					175	
323	Ser	Phe	Ser	Leu	Ser	Thr	Asn	Leu	Gln	Glu	Ser	Leu	Arg	Ser	Lys	Glu
324			180					185						190		

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 02/27/2006  
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,6,7,8,9,10,11,12,13,14

VERIFICATION SUMMARY

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TIME: 14:53:37

Input Set : F:\61310.us.sequences.ST25.txt

Output Set: N:\CRF4\02272006\J568332.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date